Supplementary Table S1

The specific primer sequences for the qRT-PCR

Gene ID	Gene symbol	Function	Forward primer (5'–3') Reverse primer (5'–3')	Amplified length (bp)
CsaV3_6G041900	*ACT7*	Actin (internal control)	TGAACTGAGATTGGTTGGCGT TTGCCCAAATCTGGAGGGTC	178
CsaV3_6G021670	*EF1α*	Elongation factor 1-alpha (internal control)	CAGACAAGCCACTCCGTCTT GCCTCGGGTAGAGATTCGTG	181
CsaV3_4G000060	*TUA*	Tubulin alpha chain (internal control)	CTCCCTCCTTTTGGAGCGTT GAAGCACAGCAACGTCAGTG	161
CsaV3_7G008500	*ABF5*	ABA responsive element binding factor	ATCACGGGCTCGTAAACAGG CATGGGCCAGTCAGTGTTCT	192
CsaV3_4G037030	*AMY2*	Alpha-amylase	GATGGGATGGTGGCCTTCAA TGCACTGAGTCACCCCATTC	180
CsaV3_5G032400	*AMY3*	Alpha-amylase	CGATTGCCCTCGATCCTCTC AGCTCTTTCGGCCATGACAA	138
CsaV3_6G002740	*ATPδ*	Delta subunit of ATP synthase	TCTACAGCCGCATTCAGCAA TGCACCTGTTTCGCGATTTG	186
CsaV3_2G032160	*ATPβ*	Beta subunit of ATP synthase	GATCGAAAAGGCCGCTCTCT AATGGCGGTGTCTCTTTCGT	139
CsaV3_1G010750	*ATPγ*	Gamma subunit of ATP synthase	TCCCAGAATTCAACCCCTGC CTCTACGGACTTTGGCAGCA	148
CsaV3_1G001830	*BADH*	Betaine aldehyde dehydrogenase	ACGTGCCAAGTATTTGCGTG TCCCATGCAGCTTCTTCCAG	111
CsaV3_3G030250	*BAM1*	Beta-amylase 1	AATGTCGCAGTCCTTCAGGG CGAACTTTGAGGCCAAACCG	159
CsaV3_4G037250	*CAT1*	Catalase	CCGAGAGGTATCCTCACCCA AAATGCTTGGCCTCACGTTG	270
CsaV3_6G031490	*CAT3*	Catalase	CACTGGAAACCAACTTGCGG ATCGTCGTATCCAACGGCTC	200
CsaV3_3G019930	*CBL4*	Calcineurin B-like protein	GAGCGAGGTAGAGGCATTGT CCATTGCGCTTCACGTCAAAT	168
CsaV3_6G039120	*CHLD*	Mg-chelatase subunit D	CCTTCAGCACAAGAATTGAAGGT CCTTGGCAAAGCCAGTTGAC	131
CsaV3_4G011730	*CHLH*	Mg-chelatase subunit H	TGTCGTCCTTGGTGTCATCG GACGAACTTCGGGACTGGTT	201
CsaV3_2G003670	*CIPK6*	CBL-interacting serine/threonine-protein kinase	GGTGGTGGAGGTGAAGAAGG CCGTCGGAGAAGTCCAAACA	107
CsaV3_1G039510	*CSD*	Cu-Zn superoxide dismutase	GCCACATTTCAACCCTGCTG GTCCACCCTTGCCAAGATCA	209
CsaV3_4G026790	*DREB2A*	Dehydration-responsive element-binding protein	ATGGCTTGGCACTTTCTCCA ACTTTCACCTTCAGTTCCTCCA	285
CsaV3_6G002010	*DREB2C*	Dehydration-responsive element-binding protein	GGAGTAGGCTTTGGCTTGGT GTGAACTCCTCAGGCACACA	259

CsaV3_2G029160	*DREB2D*	Dehydration-responsive element-binding protein	GAACCAAATCGTGGTGCTCG AGCAACATCTTCCACCGTAGG	258
CsaV3_5G028690	*FBA*	Fructose-bisphosphate aldolase	TTGTCCAGACCGCGAAATCA CAGGTGTGGTCAGCAAAAGC	156
CsaV3_5G008880	*FRB*	Fructose-1,6-bisphosphatase	TCCTTCAAAGTCAGGACGGC TATCACCTGGCCAGACTCCA	283
CsaV3_1G039270	*FSD*	Fe superoxide dismutase	TCCACTTTCCTGCTGGCTG GTAAGGATGCCTGGTGCTCT	149
CsaV3_4G023250	*GID1*	Gibberellin-insensitive dwarf	TGGTGTTCTCCGCGTTTACA CAGGTTGTGGATGGGGTCAA	127
CsaV3_7G033380	*GLYR1*	Glyoxylate reductase	TGACACCGCCAAATCCATCA TCACGACTCAGCCAAGAACC	285
CsaV3_3G009450	*GLYR2*	Glyoxylate reductase	ATCCGTCCGAGCTTGTCTTG GAACCGATCTCCCGCTGAAA	250
CsaV3_4G029990	*G6PD*	Glucose-6-phosphate 1-dehydrogenase	TCCCTGGTCTAGGAATGCGA AGCTAAGTAGTGAGCCCCGA	263
CsaV3_7G007260	*GSA*	Glutamate-1-semialdehyde 2,1-aminomutase	GGAATGGCTGGCTCTTTTGC GGGGAATTCACTCCACCAGG	206
CsaV3_2G030530	*HEMA*	Glutamyl-tRNA reductase	CACGGTGGGTAAACGGGTAA ATTCTGGCAGTGGCATGTGA	123
CsaV3_4G008050	*HEME*	Uroporphyrinogen decarboxylase	ACTATTGGTGAAGGCGGCAA GAAAGGAACGCCAAGTGCAG	247
CsaV3_1G032180	*HKT1*	High affinity K+ transporter	GTCGTCATCCACGATGGTCA ACCAAGAACATTCGTCGCCA	109
CsaV3_1G030930	*LAX*	Auxin resistant 1 (AUX1)/Like AUX1 (AUX1/LAX) influx carrier	TCTTGATGATGAGCCACCCC ATCTGAAGGTCAAGCTTACGCA	180
CsaV3_1G004740	*MSD*	Mn superoxide dismutase	AGAAGCTCCCCTGGTTGAGA CTCTCGTGGTCTCACGCATT	200
CsaV3_1G033530	*MPK3*	Mitogen-activated protein kinase	GTCCTCCGATTATGCCTATTGG TCTTAACCGCAACCATTTCGT	90
CsaV3_6G032360	*MPK6*	Mitogen-activated protein kinase	CCGTGCACCAGAGCTCTTACT CAAGGGCTTCCGATCCATTA	103
CsaV3_1G004260	*MPK9*	Mitogen-activated protein kinase	CGTGCTCCCGAACTTTGTG TTCCAGTAAGCATTTCCGCA	97
CsaV3_3G044540	*NAC35*	NAC domain-containing transcription factor	GGTCATCGTCCACGTGTTCT GCCTGAGACTGAGCAAGAGG	250
CsaV3_4G028100	*NAC41*	NAC domain-containing transcription factor	AGGGGGCAATCGAGAAACAG TGAACTCCGATGACACCACG	252
CsaV3_6G034250	*NAC66*	NAC domain-containing transcription factor	GGCGATGTGTTAATGCCGTC TCCTTCCATTTTCGCTCGCT	164
CsaV3_4G007760	*NCED2*	9-cis-epoxycarotenoid dioxygenase	GGCGATGGAATGGTTCATGC ACCGAGCTATCCCAGAGTGT	163
CsaV3_7G018780	*NHX4*	Sodium/hydrogen exchanger	AAAAACATCGGCAGCGATCA TTTTCCCCTTGCTGCAGACC	181

CsaV3_4G027860	*P5CR*	Delta-1-pyrroline-5-carboxylate reductase	GGTTGAGCCGTTACTGTGGA TCCAGCTCCGATGAACCCTA	126
CsaV3_3G034580	*P5CS*	Delta-1-pyrroline-5-carboxylate synthase	CCAAGAATGCAAGGCGTATCG CAACAGCTGCACATGCCTTT	264
CsaV3_7G004050	*PETC*	Cytochrome b6-f complex iron-sulfur subunit	CCATTGGACTTCCCACTGCT TCCATGTGCCTTCAGCCATT	146
CsaV3_3G046150	*PETE*	Plastocyanin	TTCTTACAACCATGGCCGCT ATAGCTTTGGGGATGCAGGG	129
CsaV3_5G038830	*PGD*	6-Phosphogluconate dehydrogenase	GCTGACCTCTCAGTTGCTGT TCCAAATCCGGGCAAGTTCA	283
CsaV3_3G000190	*PIN*	Auxin efflux carrier family protein	CATTTTTGGAGCGGTGGCAT GCTTTCACCTTTGACGACCG	168
CsaV3_7G003750	*PRX27*	Peroxidase	ACAATTTCACCGGCAAAGGC CGTCGAGAAGAGCGGAATCA	201
CsaV3_4G029960	*PRX47*	Peroxidase	GCAGGGGGTCCATTTTACGA TCGTAAAATGGACCCCCTGC	221
CsaV3_6G043930	*PRX73*	Peroxidase	CCTGTGCCGATATTCTCGCT GCCACAGTGTGAGAATCCGA	245
CsaV3_3G013420	*PsaD*	PSI reaction center subunit D	CTCCTTCCTCACCTCCAAGC TTTCAGCAGATTCGGCCCTT	286
CsaV3_2G010090	*PsaE*	PSI reaction center subunit E	ATGGCAATGGCTGCCTCTAA CGGAGGCACGGATAACCAAT	163
CsaV3_1G046680	*PsaF*	PSI reaction center subunit F	AAGCAATTCGCCAAGAGGGA GCACCACAAAGAAGCCCTTG	161
CsaV3_3G025000	*PsaH*	PSI reaction center subunit H	ATTTGGGCAACACCACTGGA CTGGGGCAGTAGCACTGAAA	183
CsaV3_6G052210	*PsaK*	PSI reaction center subunit K	CTCTCAGTGCTCGTTGTGGT TCTGTAGCCCAGAGTCCCTC	165
CsaV3_2G009680	*PsaL*	PSI reaction center subunit L	GAAGGAGAGCCATCTACCGC ACCGGAGATACCACCGAAGA	126
CsaV3_6G041600	*PsaN*	PSI reaction center subunit N	TCTCCTGGGGTTGTGGGTTA CCTTGCGAAGTTTGCTCCAC	249
CsaV3_6G042680	*PsbO*	PSII oxygen-evolving enhancer protein	ACCCAAAGGGAAGAGGAGGT GTCTCAGGCTTGCTCTTGGT	160
CsaV3_5G026270	*PsbP*	PSII reaction center subunit P	CCGCTTTTGTTGGGAGTTGG TGAATGCCGAATCATGGGCT	175
CsaV3_1G011330	*PsbQ*	PSII oxygen-evolving enhancer protein	GGGCTGGTAGTGGAAGCAAT TGGTGCTAGCCACACTCAAG	127
CsaV3_4G007600	*PsbR*	PSII reaction center subunit R	GCCACGTGTCTTCCTACCAA CTCGCCAGAGATGGAAGACC	218
CsaV3_2G004030	*PsbW*	PSII reaction center subunit W	TGCCCACGTTGCAAAAGATG CTCAAACCAAAAGGCAGCCC	205
CsaV3_2G001270	*PsbX*	PSII reaction center subunit X	CGGTGGAGTAGTCGTCACTG ATTTACAGCAGGAGCCGCAT	197

CsaV3_5G030690	*PsbY*	PSII core complex protein Y	CTCTTTTGCTGCCGCTCATC	240
			ACAAAACCCAAGCAATCGCC	
CsaV3_4G026530	*PYL8*	ABA receptor PYR/PYL family	GGGAGGAGACAGCATATCTAACC	139
			GGAGTGGGTTATGCGATGGG	
CsaV3_5G034360	*RBCS*	Ribulose bisphosphate	CGTGTACCGTGAGAACCACA	219
		carboxylase small chain	AATCTTGGGGGCTTGTAGGC	
CsaV3_5G008270	*RCA*	Ribulose bisphosphate	ACCCCACCAATGTCCAACTC	167
		carboxylase/oxygenase activase	GACACCGATACGGTCTTCCC	
CsaV3_7G029990	*RGL2*	DELLA protein	ACACCATTTGATTTCAGTGGCTC	95
			TCTTTCCCTCGTTGCTCTGTC	
CsaV3_6G046510	*SAMT*	salicylic acid carboxyl	CGTGGTGGACGAATGGTTGT	129
		methyltransferase	TTCCACAATCCCCTCAGCAA	
CsaV3_6G039090	*SGAT*	Serine-glyoxylate	TTCCCTTCCCACCGGAATTG	183
		aminotransferase	TCCAAAGCTGCTCTAAGCCC	
CsaV3_5G017250	*SOS1*	Na^+/H^+ antiporter	CGGTAGCATGGTTGATTTTCG	80
			GATTCGACCGGCTATGAGATG	
CsaV3_4G027060	*SOS2*	CBL-interacting protein kinase	TGTGGAACCCCTGCTTATGTC	82
			CGCACGACCAAATATCAGCTT	
CsaV3_6G048120	*SOS3*	Calcineurin B-like (CBL) protein	CAAGGAAGAGTGGCGAAACC	94
			TGGGAACGTGGTCGTGATATC	
CsaV3_6G006270	*TKL*	Transketolase	GCTGAGAAGCATTTAGCCGC	251
			ACATGCCACCCTAAAGCCTC	
CsaV3_1G001640	*TPS*	Trehalose-6-phosphate synthase	GCACCTGACTTTGTGCTGTG	185
			AGCAGGGTCAAAACATCGGT	
CsaV3_3G007160	*WRKY18*	WRKY family transcription factor	AGCGATGTTGATGTGCTGGA	233
			GTAAAGGGTTCGTGCTCCGA	
CsaV3_3G008610	*WRKY21*	WRKY family transcription factor	TCCAAACGCCGGAAGAATCA	172
			CTTGTTTTCGGGCCATGCAA	
CsaV3_6G028510	*WRKY46*	WRKY family transcription factor	GCAAGCCAAAACCAACGAGT	236
			GGACAACGAAAACGTGGTGG	

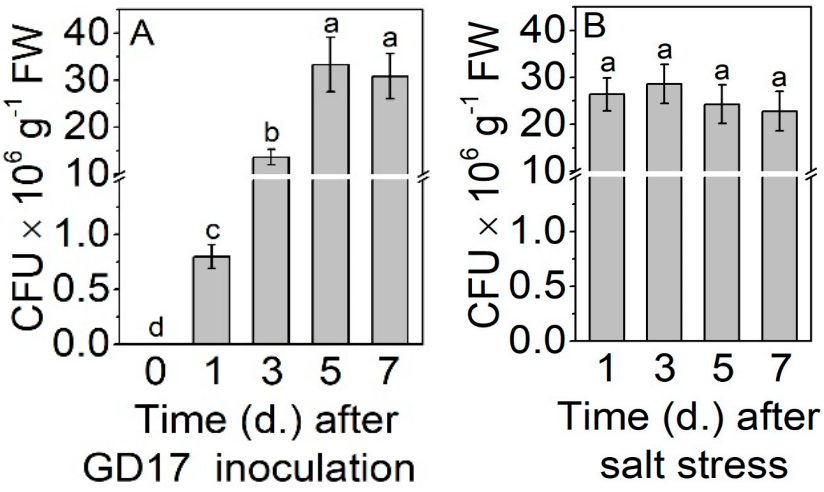


Figure S1. Colonization efficiency of GD17 inside roots as indicated by colony-forming units (CFU). GD17 inoculation was performed at 7 days after seed germination (A) and salt stress was carried out 7 days after inoculation (B). The data were collected from three replicated experiments (n = 3) with 10 plants used in each batch of experiment, and results are presented as means ± SD. Bars labeled with different lowercase letters indicate significant differences at $P < 0.05$.





Figure S2. Representative photographs illustrating the effect of GD17 inoculation on plant development. Seven-day-old seedlings were inoculated with GD17. After 28 days of inoculation (upper panel) and 48 days (lower panel), the developmental status was compared between inoculated plants and non-inoculated controls.

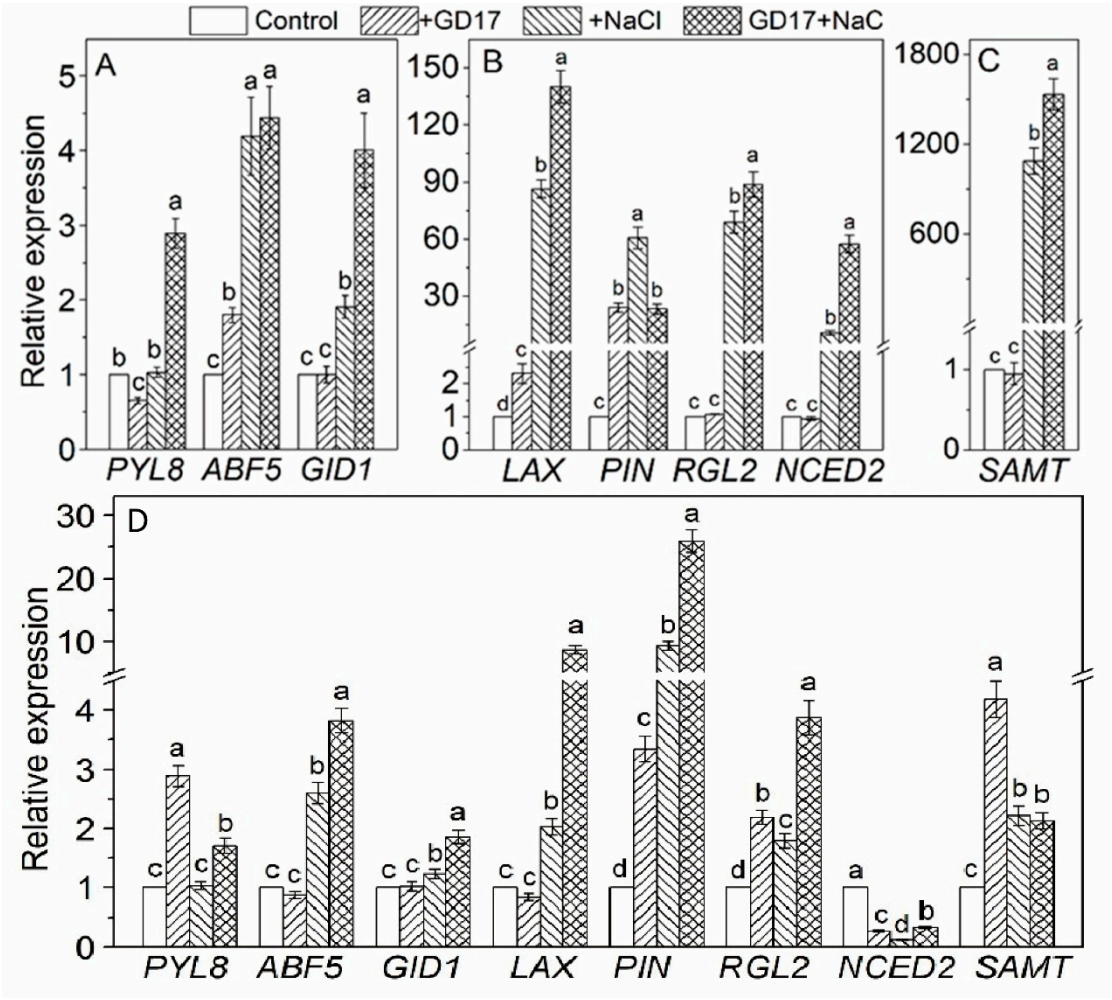


Figure S3. Effect of GD17 inoculation and/or salt stress on the expression of phytohormone synthesis and signaling-related genes in plant leaves (A-C) and roots(D). Data are presented as means ± SD from three independent experiments (n=3), with 20 seedlings per experiment. Different lowercase letters indicate significant differences at $P < 0.05$.

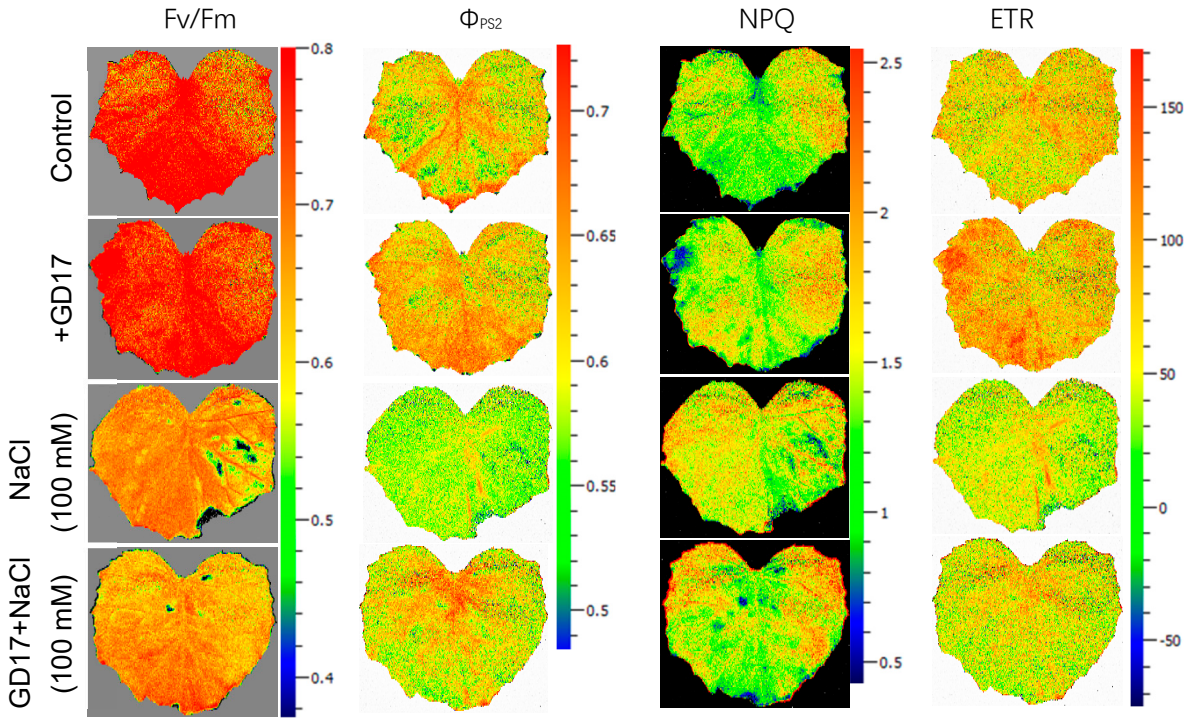


Figure S4. Representative pictures of chlorophyll a fluorescence imaging. Fv/Fm, maximum quantum efficiency of PSII; ΦPSII, actual quantum efficiency of PSII; NPQ, non-photochemical fluorescence quenching; and ETR, electron transport rate.

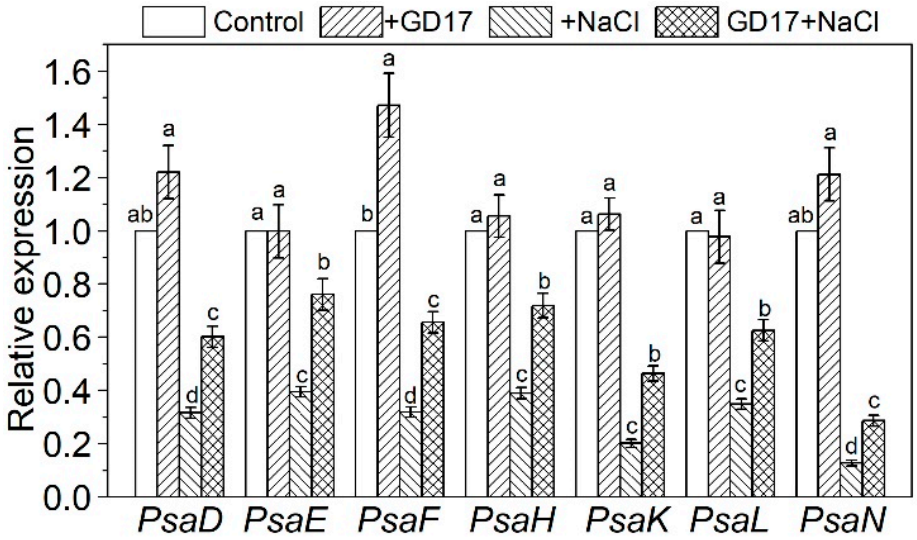


Figure S5. Effect of GD17 inoculation and/or salt stress on the expression of PSI-related genes. Data are presented as means ± SD from three independent experiments (n=3), with 20 seedlings per experiment. Different lowercase letters indicate significant differences at $P < 0.05$.

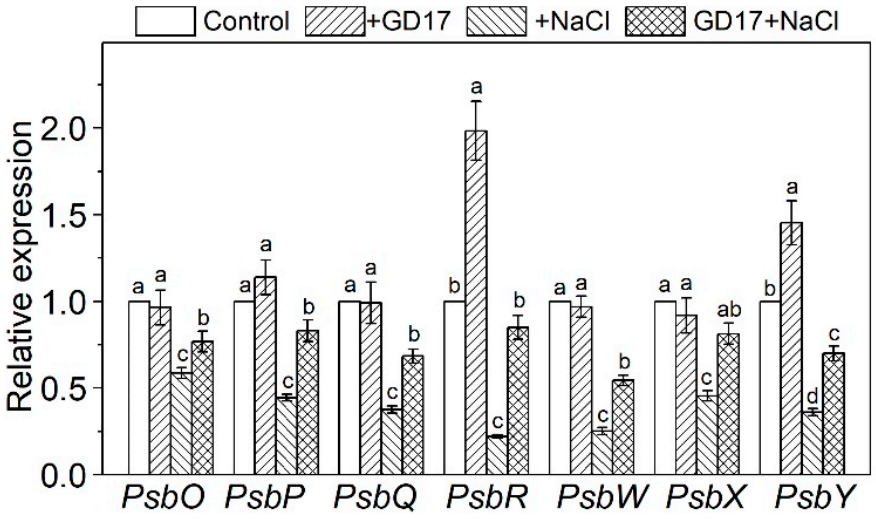


Figure S6. Effect of GD17 inoculation and/or salt stress on the expression of PSII-related genes. Data are presented as means ± SD from three independent experiments (n=3), with 20 seedlings per experiment. Different lowercase letters indicate significant differences at $P < 0.05$.

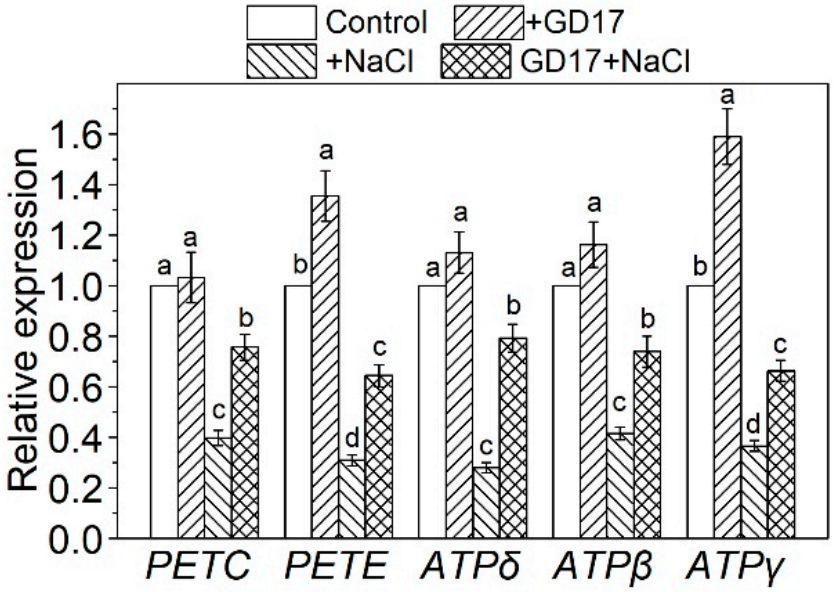


Figure S7. Effect of GD17 inoculation and/or salt stress on the expression of genes related to the electron transport and photophosphorylation. Data are presented as means ± SD from three independent experiments (n=3), with 20 seedlings per experiment. Different lowercase letters indicate significant differences at $P < 0.05$.

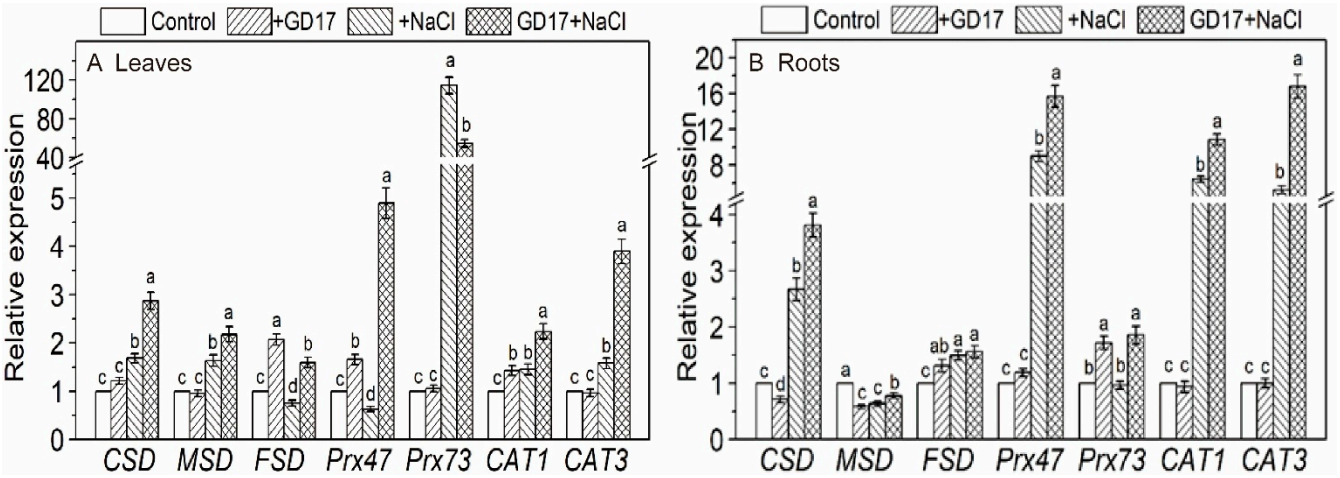


Figure S8. Effect of GD17 inoculation and/or salt stress on the expression of antioxidase-related genes in plant leaves (A) and roots (B). Data are presented as means ± SD from three independent experiments (n=3), with 20 seedlings per experiment. Different lowercase letters indicate significant differences at $P < 0.05$.